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logo

NTDB id 374 SMU RS06885 WP 002262930.1        ..MKKILIVDDEKPISDIIKFNLAKEGYDTITAFDGREALSKYEEENPDLIILDLMLPELDGLEVAKEVRKNSHVPIIML   78
NTDB id 413 AAK55817.1 141..845( )            ..MKKILIVDDEKPISDIIKFNMTKEGYEVVTAFNGREALEQFEAEQPDIIILDLMLPEIDGLEVAKTIRKTSSVPILML   78
NTDB id 606 V4T04 RS01910 WP 003130756.1      MTSKKILIIEDEKNLARFVSLELEHEGYATEIKDNGRSGLEEATSKDYDLILLDLMLPELDGFEVARRLRKEKDTPIIMM   80
NTDB id 375379 FP509 RS08445 WP 000516681.1   .MGKKILIIEDEKNLARFVSLELLHEGYDVVVETNGREGLDTALEKDFDLILLDLMLPEMDGFEITRRLQAEKTTYIMMM   79
NTDB id 471 HSISS4 RS01430 WP 002883757.1     .MSKRILIVEDEKNLARFVSLELQHEGYDVVTADNGREGLEMALEKDFDLILLDLMLPEMDGFEVTRRLQQEKDTYIMMM   79
consensus                                       !*!!!**!!!********** *!!!***** *!!**!* * ****!*!*!!!!!!!*!!*!********* **!*!*

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NTDB id 374 SMU RS06885 WP 002262930.1        SAKDSEFDKVIGLEIGADDYVTKPFSNRELLARVKAHLRRTENIESAVAEENASGIPEIIIGDLQILPDAFVAKKRGTEV   158
NTDB id 413 AAK55817.1 141..845( )            SAKDSEFDKVIGLELGADDYVTKPFSNRELQARVKALLRRSQPMPVDGQ.EADSKPQPIQIGDLEIVPDAYVAKKYGEEL   157
NTDB id 606 V4T04 RS01910 WP 003130756.1      TARDSTMDRVAGLDIGADDYITKPFAIEELLARVRAFFRREEHGHA.VERAENT.....SFRDLVIDKTNRTVHRGKKVI   154
NTDB id 375379 FP509 RS08445 WP 000516681.1   TARDSVMDIVAGLDRGADDYIVKPFAIEELLARVRAIFRRQEIETKTKEKGDSG.....SFRDLSLNTHNRSAMRGDEEI   154
NTDB id 471 HSISS4 RS01430 WP 002883757.1     TARDSIMDIVAGLDRGADDYIVKPFAIEELLARIRATFRRQDIEAAKNAPAKAS.....TYRDLKLDVQNRTVVRGDEAI   154
consensus                                     *!*!! *!*!*!!**!!!!!**!!!***!!*!!**! *!! *         *  *     ***!! *   **** ** ***

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NTDB id 374 SMU RS06885 WP 002262930.1        ELTHREFELLHHLATHTGQVMTREHLLETVWGYDYFGDVRTVDVTVRRLREKIEDTPSRPEYILTRRGVGYYMKSYD.   235
NTDB id 413 AAK55817.1 141..845( )            DLTHREFELLYHLASHTGQVITREHLLETVWGYDYFGDVRTVDVTVRRLREKIEDTPSRPEYILTRRGVGYYMRNNA*   234
NTDB id 606 V4T04 RS01910 WP 003130756.1      DLTRREYDLLLTLMQNVGDVVTREHLVSQVWGYEEGTETNVVDVYIRYLRNKI.DVEGQDSYIQTVRGLGYVMRERK.   230
NTDB id 375379 FP509 RS08445 WP 000516681.1   SLTKREFDLLNVLMTNMNRVMTREELLEHVWKYDVAAETNVVDVYIRYLRGKI.DIPGRESYIQTVRGMGYVIREK..   229
NTDB id 471 HSISS4 RS01430 WP 002883757.1     PLTKREFDLLNTLLSNMNQVMTREELLLQVWKYDDAIETNVVDVYIRYLRGKI.DVPGKESYIQTVRGMGYVIREK..   229
consensus                                     *!!*!!**!!  !******!*!!!*!** !!*!* ***********!*!! !! !******!!*!*!!*!!*****
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X non conserved

X similar

X $\geq$ 50% conserved